For the Examiner's convenience, all pending claims are shown below.

1. (Currently Amended) An array comprising a plurality of polynucleotide probes immobilized on a solid support, wherein:

(a) the plurality of polynucleotide probes corresponds to a multiplicity of gene transcripts and comprises at least 100 polynucleotides that are each complementary to a distinct gene transcript;

(b) each polynucleotide probe of the plurality is localized to a predetermined region on the solid support;

(c) each polynucleotide probe of the plurality is from about 50 to 500 nucleotides in length;

(d) each polynucleotide probe of the plurality is complementary to 3' untranslated sequence of a gene transcript, the [~~said~~] untranslated sequence having a defined chromosomal location; and

(e) each polynucleotide probe of the plurality is prepared by amplification of genomic DNA or cDNA using a primer pair selected from the group consisting of SEQ ID NOS. 1-2, 3-4, 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, and 67-68.

2. (Previously Amended) An array of claim 1, wherein each polynucleotide probe of the plurality of polynucleotide probes is from about 50 to 400 nucleotides in length.

3. (Previously Amended) An array of claim 1, wherein each polynucleotide probe of the plurality of polynucleotide probes is from about 50 to 300 nucleotides in length.

4. (Original) An array of claim 1, wherein the predetermined region comprises at least 2 single-stranded polynucleotides that are complementary to the same gene transcript.

5. (Original) An array of claim 1, wherein the predetermined region comprises at least 100 single-stranded polynucleotides that are complementary to the same gene transcript.

6. (Original) An array of claim 1, wherein the predetermined region comprises at least 2 single-stranded polynucleotides of identical sequences.

7. (Original) An array of claim 1, wherein the predetermined region comprises at least 100 single-stranded polynucleotides of identical sequences.

8. (Original) An array of claim 1, wherein the predetermined region has an average size ranging from about 0.01 cm^2 to about 1 cm^2.

9. (Original) An array of claim 1, wherein the plurality of polynucleotide probes is immobilized to the solid support via a covalent linkage.

10. (Original) An array of claim 1, wherein the solid support is flexible.

11. (Original) An array of claim 1, wherein the solid support is rigid.

12. (Original) An array of claim 10, wherein the solid support is made of one or more substances selected from the group consisting of nitrocellulose, nylon, polypropylene, glass, and silicon.

13. (Original) An array of claim 11, wherein the solid support is made of one or more substances selected from the group consisting of nitrocellulose, nylon, polypropylene, glass, and silicon.

14. (Original) An array of claim 1, further comprising a control probe.

15. (Original) An array of claim 14, wherein the control probe is selected from the group consisting of normalization control probe, expression level control probe, and mismatch control probe.

16. (Currently Amended) An array of claim 14, wherein the control probe has [~~having~~] sequence[~~s~~] complementary to one or more constitutively expressed genes.

17. (Previously Amended) An array of claim 1, wherein each polynucleotide probe of the plurality is prepared by amplification of genomic DNA or cDNA using a pair of primers that amplify the region corresponding to 3' untranslated sequence of a gene transcript.

18. (Currently Amended) An array of claim 1, wherein the array comprises a polynucleotide probe prepared by amplification of genomic DNA or cDNA using a primer pair selected from the group consisting of SEQ ID NOS. 1-2, 3-4, 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, and 67-68 and includes at least one control probe.

19. (Previously Amended) An array of claim 1 further comprising target polynucleotides corresponding to gene transcripts expressed in a subject, wherein the target polynucleotides are bound to the polynucleotide probes in form of stable target-probe hybridization complexes.

20. (Original) An array of claim 19, wherein the target polynucleotides are conjugated with a detectable label selected from the group consisting of an enzyme, a radioactive and a luminescent substance.

21. (Original) An array of claim 19, wherein the target polynucleotides are DNA or RNA molecules.

22. (Original) An array of claim 19, wherein the target polynucleotides are cDNAs.

23. (Currently Amended) A method of preparing an array of polynucleotide probes corresponding to a multiplicity of gene transcripts, the [~~said~~] method comprising:

(a) generating a plurality of gene-specific polynucleotides by amplification of genomic DNA or cDNA using a primer pair selected from the group consisting of SEQ ID NOS. 1-2, 3-4, 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, and 67-68, wherein each polynucleotide of the plurality is from about 50 to about 500 nucleotides in length, and wherein each polynucleotide is complementary to 3' untranslated sequence of a gene transcript, the [~~said~~] untranslated sequence having a defined chromosomal location;

(b) immobilizing the plurality of polynucleotides in a predetermined region on a solid support; and

(c) repeating steps (a) and (b) to yield an array of polynucleotide probes corresponding to a multiplicity of gene[s] transcripts.

69. (New) A method of using an array to detect gene expression in a sample, the method comprising:

(a) contacting the polynucleotide probes of the array of claim 1 with labeled target polynucleotides from the sample under conditions to form stable target-probe complexes; and

(b) detecting complex formation, thereby detecting gene expression in the sample.